Fig. 1

Nucleotide Sequence of the Clone #10

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          10         20         30         40         50         60         70         80         90        100
          |          |          |          |          |          |          |          |          |          |
   1 GCCACGAAGG CCCAGACTTT GACCGTTCTT CACCACCACT CCAGCCTCCT CCTGTGAACT CACTGACCAC CGAGAACCAGA TCCACTCTT TACCATTCAG  100
 101 TCTCACCAAG ATGCCCAAATA CCAATGGAAG TATTGGCCAC AGTCCACTTT CTCTGTCGAC CCAGTCTGTA ATGGAAGAGC TAAACACTGC ACCCGTCCAA  200
 201 GAGAGTCCAC CCTTGGCCAT GCCTCCTGGG AACTCACATG GTCTAGAAGT GGGCTCATTG GCTGAAGTTA AGGAGAACCC TCCTTTCTAT GGGGTAATCC  300
 301 GTTGGATCGG TCAGCCACCA GGACTGAATG AAGTGCTCGC TGGACTGGAA CTGGAAGATG AGTGTGCAGG CTGTACGGAT GGAACCTTCA GAGGCACTCG  400
 401 GTATTCACC TGTGCCCTGA AGAAGGCGCT GTTTGTGAAA CTGAAGAGCT GCAGGCCTGA CTCTACGGTTT GCATCATTGC AGCCGGTTTC CAATCAAGAT  500
 501 TGAGCGCTGT AACTCTTTAG CATTGGGAGG CTACTTAAGT GAGTACTT;G AAGAAAATAC T:CCA:CCAA AAATGGAAAA AGAARGCTTG GAGATAATGA  600
 601 TTGGGGAAAG AAGAAAGGCA TCCAAGGGTC ATTACAATTC TTGKTACTTA G:ACTCAACC TTATTKGCT TTTAGTTCTG TTCTNGGACA  700
 701 CTGGTGTTAC TTTAGACCCC AAAGAAAAG AAAGCATGTT AGAATATWT KKKGNMGCCC AACAGCTACT GAGGACAGAA ATTGTTAATC CTCTGAGAAT  800
 801 ATATGGATAT GTGTGTGCCA CAAAATATAT GAAACTGAGG AAATACTTG AAAAAGTGGA GGCTGCATCA GGATTTACCT CTGAAGAAAA AGATCCTGAG  900
 901 GAATTCTTGA ATATTCTGTT TNATCATATT TTAAGGGTAG AACCTTTGCT AAAAAATAGA TCAGCAGGTC AAAAGGTACA TCTATCAAA 1000
1001 TTTTTATNGA AAAAAATGAG AAAGTTGGCG TTCCCACAAT TCAGCAGTTG TTGAATGGT CTTTATCAA CAGTACCCTG AAATTGCAG AGGCACCATC 1100
1101 ATGTCTGATT ATTCAGATGC CTCGATTTGG AAAAGACTTT AAACTATTTA AAAAATTTTT CCTTCTCTGG AATTAGATAT AACAGATTTA CTTGAAGACA 1200
1201 CCCCAGACAG TGCCGGATAT GTGGAGGGCT TGCAATGTAT GAGTGTAAGA ATGCTACGAC GATCCGGACA CCAGCTGGAA AAACAAGCAG TTTTGTAAAA 1300
1301 CCTGCAACAC TCAAGTCCAC CTTCATCCGA AGAGGCTGAA TCATAAATAT AACCCAGTGT CACTTCCCAA AGACTTACCC CGACTGGGAG ATTGGAGACA 1400
1401 CGGCTGCCATC CCTTGCCAGA ATATGAGTT ATTTGCTGTT CTCTGCATAG AAACAAGCCA CTATGTTGCT TTTGTGAAGT ATGGGAAGGA CGATTCTGCC 1500
1501 TGGCTCTTCT TTGGCACAGCA TGGCCGATCC GGGATGGTGG TCAGAAATGC CCCAAGTCAC CCHTGSCCCA GAAGTAGGAG AGTACTTGGA 1600
1601 AGATGTCTCC TGGAAGACCC TGSAWTYCCT TGGACTCCCA GGAGAATCCC AAGGTGTGC ACGAAGACTG CTTTGTGATG CCATATATGT GCCATGTACC 1700
1701 CAGAGTCCAA CAATGAGTTT GTACAAATAA CTGGGGGTCA TCGGGGAAAGG CAAAGAAACT GGAAGGCAGA GTCCCTAACG TTGCATCTTA TTCGGAGCTG 1800
1801 GCAGTTCTGT TCACGGTCCA TTGCCGGCAA TGGATGTCTT TGTGGTGATG ATCCTTCAGA AAAGGAATGCC TCTGTTTAAA AACAAATTGC TTTTGTGTGCC 1900
1901 CTGAAGTATT TAATAAGAAG CATTTTGCAC TCTAGAAAGT ATGTTGTGT AGAAGTCTAA ATGAAGTTAT TAATACCTGA AGCTTTAAGT 2000
2001 TAAGTGCATT GATCATANGA TATTTTTGGA AGCATACAAT TTTAATTGTC GAAGTTTAAA GCCTCTTTTA GTCCATTGAG AATGTAAATA AATGTGTCYT 2100
2101 CTTTATNGGAA AAAAAA                                                                                           2116
          |          |          |          |          |          |          |          |          |          |
          10         20         30         40         50         60         70         80         90        100
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Fig. 2

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   1 GGGGTTTTCT TTTACACCTC TCGGTACCG  AACTCGGATC CACTAGTAAC GGGCCGCCAG TGTGCTGAA ATTCGGCACG AGGGTGTGG GAGCCGGGGC 100
 101 CGGCCCGGGA CGCGGGCTGG GGAGCCGGGG CGAGGGGCGA CGCCCCGCCG CCCGAGTTTC GGGTGAGGAT GGTTCTACAC AGCCACCCGG 200
 201 AGTTCCTTAG TTGAAAGGTG CGCCCTGCTG TGACAGAATG TGGTAATTGT AAACATATT CATCTTAATA CAACATGAC ACCACGTTGC TGAAAACATG 400
 301 TCTTCATGGA AAATTGATAA ATATTTGTGC CTTCCAACTC TCGTCTTGGT TGAATGACTT CATCTTAATA CAACATGAC ATCACAATGA 500
 401 CTTTGGGACT GCCACTGAAT TTATCTTTTG CGGTTTTATG  ACAAAGTTAT TAGTAGTTTC CCTTTTTTGA ATTAGTATTT TGAAGTTAAT ATCACAATGA 500
 501 GTTCAGGCTT ATGGAGCCAA GAAAAAGTCA CTTCACCCTA CTGGGAAGAG CGGATTTTTT ACTTGCTTCT TCAAGAATGC AGCGTTACAG ACAAACAAAC 600
 601 ACAAAAGCTC CTTAAAGTAC CGAAGGGAAG TATAGGACAG TATATTCAAG ATCGTTCTGT GGGGCATTCA AGGATTCCTT CTGCAAAAGG CAAGAAAAAT 700
 701 CAGATTGGAT TAAAAATTCT AGAGCAACCT CATGCAGTTC TCTTTGTTGA TGAAATGGAT GTTGTAGAGA TAAATGAAAA GTTCACAGAG TTACTTTTGG 800
 801 CAATTACCAA TTGTGAGGAG AGGTTCAGCC TGTTTAAAAA CAGAAACAGA CTAAGTAAAG GCCTCCAAAT AGACGTGGGC TGTCCTGTGA AAGTACAGCT 900
 901 GAGATCTGGG GAAGAAAAAT TTCCTGGAGT TGTACGCTTC AGAGGACCCC GAGGACAGTC TCCGGAATAT TCTTTGGAGT TGAATTGCTG 1000
1001 GAAGAAGGTC GTGGTCAAGG TTTCACTGAC GGGGTGTACC AAGGGAAACA GCTTTTTCAG TGTGATGAAG ATTGTGGCGT TTGGACAAGC TAAACTCCAG 1200
1101 TAGAACTCAT AGAAGATGAT GACACTGCAT TGGAAAGTGA TTACGCAGGT CCTGGGGACA CAATGCAGGT CGAACTTCCT CCTTTGGAAA TAAACTCCAG 1200
1201 AGTTTCTTTG AAGGGTGGAG AAACAATAGA ATCTGAACA GTTATATTCT GTGATGTTTT GCGTGTGTTG AAAGTACAAT TCTATTGCAC ATCAATGATA 1400
1301 ATGGATAACC CTATTGGCAA CTGGGATGGA AGATTTGATG GAGTGCACT TTGTAGTTTT GCGTGTGTTG AAAGTACAAT TCTATTGCAC ATCAATGATA 1400
1401 TCAATCCAGA GAGTGTGACG CAGGAAAGGA GGCCTCCCAA ACTTGCCTTT ATGTCAAGAG GTGTTGGGGA CAAAGGTTCA TCCAGTCATA ATAAACCAAA 1500
1501 GGCTACAGGA TCTACCTCAG ACCCTGGAAA TAGAAMCAGA TCTGAATTAT TTTATACCTT AAATGGGTCT CACAACCACA ATCCAAATCA 1600
1601 AAAAATACAT GGTACATTGA TGAAGTTGCA GAAGACCCTG CAAAATCTCT TACAGAGATA TCTACAGACT TTGACCGTTC TTCCACCACA CTCCAGCCTC 1700
1701 CTCCTGTGAA CTCCACTGACC ACCGAGAACA GATTCCACTC TTTACCATTC AGTCTCACCA AGATGCCCAA TACCAACTGA AGTATTGGCC ACAGTCCACT 1800
1801 TTCTCTGTCA GCCCAGTCTG TAATGGAAGA GCTAAACACT GCACCCGTCC AAGAGAGTCC ACCCTTGGCC ATGCCTCCTG GGAACTCACA TGGTCTAGAA 1900
1901 GTGGGCTCAT TGGCTGAAGT TAAGGAGAAC CCTCCTTTCT ATGGGGTAAT  CCGTTGGATC GGTCAGCCAC CAGGACTGAA TGAAGTGCTC GCTGGACTGG 2000
2001 AACTGGAAGA TGAGTGTGCA GGCTGTACGG ATGGAACCTT CAGAGGCACT CCTGTGCCCT GAAGAAGGCG CTGTTTGTGA AACTGAAGAG 2100
2101 CTGCAGGGCT GACTCTAGGT TTGCATCATT GCAGCCGGTT TCCAATCAGA TTGAGCGCTG TAACTCTTTA GCTACTTAAG TGAAGTAGTA 2200
2201 GAAGAAAATA CTCCACCAAA AATGGAAAA GAAGGCATCC AGGGTCATTA TGGGAAGAAG AAAGGCATCC AGGGTCATTA CAATTCTTGT TACTTTAGACT 2300
2301 CAACCTTATT CTGCTTATTT GCTTTAGTT CTGTTCTGGA CACTGTGTTA CTTAGACCCA  AGAAAAGAA CGATGTAGAA TATTATAGTG AAACCCAAGA 2400
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2401 GCTACTGAGG ACAGAAATTG TTAATCCTCT GAGAATATAT GGATATGTGT GTGCCACAAA AATTATGAAA CTGAGGAAAA TACTTGAAAA GGTGGAGGCT 2500
2501 GCATCAGGAT TTACCTCTGA AGAAAAAGAT CCTGAGGAAT TCTTGTTCAT CATATTTAA GGGTAGAACC TTTGCTAAAA ATAAGATCAG 2600
2601 CAGGTCAAAA GGTACAAGAT TGTTACTTCT ATCAAATTTT TATGGAAAAA AATGAGAAAG TTGGCGTTCC CACAATTCAG CAGTTGTTAG AATGGTCTTT 2700
2701 TATCAACAGT AACCTGAAAT TTGCAGAGGC ACCATCATGT CTGATTATTC AGATGCCTCG ATTTGGAAAA GACTTTAAAC TATTTAAAAA AATTTTTCCT 2800
2801 TCTCTGGAAT TAAATATAAC AGATTTACTT GAAGACACTC CCGGATATGT GGAGGGCTTG CAATGTATGA GTGTAGAGAA TGCTACGACG 2900
2901 ATCCGGACAT CTCAGCTGGA AAAATCAAGC AGTTTTGTAA AACCTGCAAC ACTCAAGTCC ACCTTCATCC GAAGAGGCTG AATCATAAAT ATAACCCAGT 3000
3001 GTCACTTCCC AAAGACTTAC CCGACTGGGA CTGGAGACAC GGCTGCATCC CTTGCCAGAA TATGGAGTTA TTTGCTGTTC TCTGCATAGA AACAAGCCAC 3100
3101 TATGTTGCTT TTGTGAAGTA TGGGAAGGAC GATTCTGCCT GGCTCTTCTT TGACAGCATG GCCGATCGGG ATGGTGGTCA GAATGGCTTC AACATTCCTC 3200
3201 AAGTCACCCC ATGCCCAGAA GTAGGAGAGT ACTTGAAGAT GTCTCTGGAA GACCTGCATT CCTTGGACTC CAGGAGAATC CAAGGCTGTG CACGAAGACT 3300
3301 GCTTTGTGAT GCATATATGT GCATGTACCA GAGTCCAACA ATGAGTTTGT ACAAATAACT GGGGTCATCG GGAAAGGCAA AGAAACTGAA GGCAGAGTCC 3400
3401 TAACGTTGCA TCTTATTCGA GCTGGCAGTT CTGTTCACGT CCATTGCCGG CAATGGATGT CTTTGTGGTG ATGATCCTTC AGAAAAGGAT GCCTCTGTTT 3500
3501 AAAAACAAAT TGCTTTTGTG TCCCTGAAGT ATTTAATAAG AAGCATTTTG CACTCTAGAA AGTATGTTTG TTAAGAAGTC TAAATGAAGT 3600
3601 TATTAATACC TGAAGCTTTA AGTTAAGTGC ATTGATCATA TGATATTTTT GGAAGCATAC AATTTTAATT GTGGAAGTTT AAGCCTCTCTT TTAGTCCATT 3700
3701 GAGAATGTAA ATAAA 3715

Fig. 2 (cont.)

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  8     MSS GLNSQEKVTS PYWEERIFYL LLQECSVTDK QTQKLLKVPK GSIGQYIQDR SVGHSRIPSA KGKKNQIGLK ILEQPHAVLF VDEDVVEINE  100
101 KFTELLLAIT NCEERFSLFK NRNRLSKGLQ IDVGCPVKVQ LRSGEEKFPG VVRFRGPLLA ERTVSGIFFG VELLEEGRGQ GFTDGVYQGK QLFQCDEDCG  200
201 FVALDKLEL  IEDDTALES  DYAGPGDTMQ VELPPLEINS RVSLKGGETI ESGTVIFCDV LPGKESLGYF VGVDMDNPIG NWDGRFDGVL CSFACVESTI  300
301 LLHINDIIPE SVTQERRPPK LAFMSRGVGD KGSSSHNKPK ATGSTSDPGN RRSELFYTLN GSSVDSQFQS KSKNTWYIDE VAEDPAKSLT EISTDFDRSS  400
401 PPLQPPPVNS LTTENRFHSL PFSLFRMPNT NGSIGHSPLS LSAQSVMEEL NTAPVQESPP LANPPGNSHG LEVGSLAEVK ENPPFYGVIR WIGQPPGLNE  500
501 VLAGLELEDE CAGCTDGTFR GTRYFTCALK KALFVRLKSC RPDSRFASLQ PVSNQIERCN SLAFGGYLSE VVEENTPPKM EKEGLEIMIG KKKGIQGHYN  600
601 SCYLDSTLFC LFAFSSVLDT VLLRPKEKND VEYYSETQEL LRTEIVNPLR IYGYVCATKI MKLRKILEKV EAASGFTSEE KDPEEFLNIL FHHILRVEPL  700
701 LKIRSAGQKV QDCYFYQIEM ERNEKVGVPT IQQLLEWSF! NSNLKFAEAP SCLIIQMRFE GKDEKLFKKI FPSLELNITD LLEDTPRQCR ICGGLAMYEC  800
801 RECYDPDIS  AGKLKQFCKT CNTQVHLHPK RLNHKYNPVS LPKDLPDWDW RHGCIPCQNM ELFAVLCIET SHYVAFVKYG KDDSAWLFFD SMADRDGGQN  900
901 GENIPQVTPC PEVGEYLKNS LEDLHSLDSR RIQGCARRLL PTMSLYK                                                           957
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Fig. 3